Luke R. Thompson, Ph.D.

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Research Associate
Northern Gulf Institute, USM
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Lecturer
Scripps Institution of Oceanography
University of California, San Diego

AREAS OF INTEREST

Microbial roles in health and environment, microbial ecology and evolution, genomics and metagenomics, transcriptomics and metatranscriptomics, bioinformatics, biostatistics, and data visualization.

EDUCATION

STANFORD UNIVERSITY, *Stanford, California*

B.S.	Biological Sciences *with Honors*	1998–2002
	Chemistry *Minor*	

MASSACHUSETTS INSTITUTE OF TECHNOLOGY, *Cambridge, Massachusetts*

Ph.D.	Biology	2003–2010
	Microbiology *Specialization*	

POSTDOCTORAL POSITIONS

KING ABDULLAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, *Thuwal, Saudi Arabia*

Postdoctoral Fellow	Red Sea Research Center	2010–2013

UNIVERSITY OF COLORADO, *Boulder, Colorado* & UNIVERSITY OF CALIFORNIA, *San Diego, California*

Postdoctoral Scholar	Rob Knight Lab	2013–2016

PUBLICATIONS

25. **Thompson LR**, et al. The Earth Microbiome Project: Biogeography of microbial taxa and communities on Earth. In preparation for submission to *Nature*.

24. Franzosa EA, McIver LJ, Rahnavard G, **Thompson LR**, Schirmer M, Weingart G, Schwarzberg Lipson K, Knight R, Caporaso JG, Segata N, Huttenhower C. Functionally profiling metagenomes and metatranscriptomes at species-level resolution. In review, *Nature Biotechnology*.

23. Duarte B, Goodwin KD, **Thompson LR**, Marques JC, Kahlke T, and Caçador I. Metagenomic approaches to the new challenges in marine ecological quality assessments. In revision, *Frontiers in Marine Science*.

22. Debelius JW, McDonald D, ..., **Thompson LR**, ..., The American Gut Consortium, and Knight R. American Gut: An open platform for citizen-science microbiome research. In revision, *Science*.

21. **Thompson LR**, Nikolakakis K, Pan S, Reed J, Knight R, and Ruby EG. Transcriptional characterization of *Vibrio fischeri* during colonization of juvenile *Euprymna scolopes*. In press, *Environmental Microbiology*.

20. Amir A, McDonald D, Navas-Molina J, Kopylova E, Morton J, Xu ZX, Kightley EP, **Thompson LR**, Hyde ER, Gonzalez A, and Knight R. Deblur rapidly resolves single-nucleotide community sequence patterns. In press, *mSystems*.

19. **Thompson LR**, Zeng Q, and Chisholm SW. Gene expression patterns during light and dark infection of *Prochlorococcus* by cyanophage. *PLOS ONE* 11(10):e0165375, doi:10.1371/journal.pone.0165375, 2016.

18. **Thompson LR**, Williams GJ, Haroon MF, Shibl A, Larsen P, Shorenstein J, Knight R, and Stingl U. Metagenomic covariation along densely sampled environmental gradients in the Red Sea. *The ISME Journal*, doi:10.1038/ismej.2016.99, 2016.

17. Haroon MF, **Thompson LR**, Parks DH, Hugenholtz P, Stingl U. A catalogue of 136 microbial draft genomes from the Red Sea. *Scientific Data*, doi:10.1038/sdata.2016.50, 2016.

16. Shibl A, Haroon MF, Ngugi DK, **Thompson LR**, Stingl U. Distribution of *Prochlorococcus* ecotypes in the Red Sea basin based on analyses of *rpoC1* sequences. *Frontiers in Marine Science*, doi:10.3389/fmars.2016.00104, 2016.

15. Haroon MF, **Thompson LR**, Stingl U. Draft genome sequence of uncultured SAR324 bacterium lautmerah10, binned from a Red Sea metagenome. *Genome Announcements* 4(1):e01711-15, doi:10.1128/genomeA.01711-15, 2016.

14. Metcalf JL, Xu Z, Weiss S, Lax S, Van Treuren W, Hyde ER, Song S, Amir A, Larsen P, Sangwan N, Haarmann D, Humphrey GC, Ackermann G, **Thompson LR**, Lauber C, Bibat A, Nicholas C, Gebert MJ, Petrosino JF, Reed SC, Gilbert JA, Lynne AM, Bucheli SR, Carter DO, and Knight R. Microbial community assembly and metabolic function during mammalian corpse decomposition. *Science* 351:158–162, 2016.

13. Luo H, **Thompson LR**, Stingl U, and Hughes AL. Selection maintains low genomic GC content in marine SAR11 lineages. *Molecular Biology and Evolution*, doi:10.1093/molbev/msv149, 2015.

12. Berube PM, Biller SJ, Kent AG, Berta-Thompson JW, Roggensack SE, Roache-Johnson KH, Ackerman M, Moore LR, Meisel JD, Sher D, **Thompson LR**, Campbell L, Martiny AC, and Chisholm SW. Physiology and evolution of nitrogen acquisition in *Prochlorococcus*. *The ISME Journal* 9:1195–1207, 2015.

11. Shibl AA, **Thompson LR**, Ngugi DK, and Stingl U. Distribution and diversity of *Prochlorococcus* ecotypes in the Red Sea. *FEMS Microbiology Letters*, doi:10.1111/1574-6968.12490, 2014.

10. **Thompson L**. Red Sea Metagenomics. In: Nelson K (Ed.) *Encyclopedia of Metagenomics: SpringerReference*. Springer-Verlag, Berlin Heidelberg, 2013.

9. **Thompson LR**, Field C, Romanuk T, Ngugi DK, Siam R, El Dorry H, and Stingl U. Patterns of ecological specialization among microbial populations in the Red Sea and diverse oligotrophic marine environments. *Ecology and Evolution* 3:1780–1797, 2013.

8. Stingl U, Ngugi DK, **Thompson L**, Antunes A, and Cahill M. Mikrobielle Ökologie des Roten Meeres. *BIOspektrum* 18:582–584, 2012.

7. **Thompson LR**, Zeng Q, Kelly L, Huang KH, Singer AU, Stubbe J, and Chisholm SW. Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism. *Proc Natl Acad Sci USA* 108:E757–E764, 2011.

    - *Selected by Faculty of 1000 as a "must read" article with a FFa score of 8.*
    - *PNAS Plus Author Summary associated with this article.*

6. **Thompson LR**. Auxiliary metabolic genes in viruses infecting marine cyanobacteria. Ph.D. Thesis, Massachusetts Institute of Technology, 2010.

5. Sullivan MB, Huang KH, Ignacio-Espinoza JC, Berlin A, Kelly L, Weigele PR, DeFrancesco AS, Kern SE, **Thompson LR**, Young S, Lee W, Weiand M, Fu R, Krastins B, Chase M, Sarracino D, Osburne MS, Henn MR, and Chisholm SW. Genomic analysis of oceanic cyanobacterial myoviruses compared to T4-like myoviruses from diverse hosts and environments. *Environmental Microbiology* 12:3035–3056, 2010.

4. Zinser ER, Lindell D, Johnson ZI, Futschik ME, Steglich C, Coleman ML, Wright MA, Rector T, Steen R, McNulty N, **Thompson LR**, and Chisholm SW. Choreography of the transcriptome, photophysiology, and cell cycle of a minimal photoautotroph, *Prochlorococcus*. *PLOS ONE* 4(4):e5135, 2009.

3. Elmer KR, **Thompson LR**, and Meyer A. Similar levels of diversity and population structure in superflock and non-superflock cichlid fishes from Lake Victoria, Africa. *Trop Freshwater Biology* 18(2):1–14, 2009.

2. Breitbart M, **Thompson LR**, Suttle CA, and Sullivan MB. Exploring the vast diversity of marine viruses. *Oceanography* 20(2):135–9, 2007.

1. Sullivan MB, Lindell D, Lee JA, **Thompson LR**, Bielawski J, and Chisholm SW. Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts. *PLOS Biology* 4(8):e234, 2006.

Invited Talks

12. GRDI-Ecobiomics: Workshop on Environmental and Protocol Metadata, Ottawa, May 2016. "Environmental metadata and the Earth Microbiome Project."

11. Sharp HealthCare Obesity Crisis Conference, San Diego, May 2016. "Healthy gut and microbiomes."

10. Microbiome Connections to the Environment and Health, Calit2, Irvine, September 2015. "Computational tools for environmental genomics and the Earth Microbiome Project."

9. Scripps Institution of Oceanography, February 2015. "Metagenomic analysis and the Earth Microbiome Project."

8. 2nd International Symposium on Sponge Microbiology, Baltimore, October 2014. "The Earth Microbiome Project: Early successes and challenges" and panel member of "Group discussion: Where to from here?"

7. 15th International Symposium on Microbial Ecology, Seoul, August 2014. "Mapping the genetic diversity and physicochemical space of the Red Sea basin."

6. Pacific Northwest National Laboratory, November 2013. "Marine metagenomics: The Red Sea and the Earth Microbiome Project."

5. Woods Hole Oceanographic Institution, July 2012. "Let my microbes go! The Red Sea and stress tolerance strategies of *Prochlorococcus*, cyanophage, and SAR11."

4. Winter Enrichment Program, KAUST, January 2012. "The coming big data singularity."

3. Integrative Microbial Ecology Workshop, KAUST, June 2010. "Auxiliary metabolic genes in viruses infecting marine cyanobacteria."

2. DOE Genomics:GTL (Genomes-To-Life) Contractor–Grantee Workshop VII, Bethesda, February 2009. "Viruses hijacking cyanobacterial carbon metabolism."

1. Boston Bacterial Meeting, June 2007. "Transaldolase in viruses infecting *Prochlorococcus*: Hijacking host carbon metabolism with a non-cyanobacterial enzyme."

Awards & Honors

- SABIC Postdoctoral Fellowship, King Abdullah University of Science and Technology, 2012
- SABIC Postdoctoral Fellowship, King Abdullah University of Science and Technology, 2011
- Poster Award, Cells, Circuits, and Computation Conference, Harvard, 2009
- Student Travel Grant, Genomics: GTL Conference, U.S. Department of Energy, 2009
- Praecis Presidential Fellowship, Massachusetts Institute of Technology, 2003
- Howard Hughes Summer Research Fellowship, Stanford Department of Biological Sciences, 2001
- Semifinalist, Westinghouse Science Talent Search, 1998

Research Cruises

- KAUST Red Sea Expedition 2013. "Gene expression of marine bacterial communities in the Eastern Mediterranean and Northern Red Sea." *R/V Aegaeo*, Feb 14–Mar 6 and Mar 9–17, 2013.
- KAUST Red Sea Expedition 2011. "Population genomics of marine bacteria along physicochemical gradients in the Eastern Red Sea." *R/V Aegaeo*, Sept 15–Oct 10, 2011.
- Hawaii Ocean Time-series HOT-181. "Cultivation of *Prochlorococcus* from the North Pacific Subtropical Gyre." *R/V Kilo Moana*, May 24–29, 2006.

Peer Review

- Review Editor for *Marine Molecular Biology and Ecology*
- Reviewer for *Nature*, *Ecology Letters*, *The ISME Journal*, *Bacteriophage*, National Science Foundation, United States–Israel Binational Science Foundation

Laboratory Skills

Microbiology

- Culturing of marine bacteria and viruses
- Genetic manipulations of bacteria

Molecular biology
- Molecular cloning
- High-throughput PCR, sequencing, and qPCR
- Next-generation sequencing: 454, Illumina, RNA-Seq

Protein biochemistry
- Protein expression, purification, detection, and structure determination
- Biochemical assay design and implementation
- Steady-state enzyme kinetics

Computational Skills

Data science, statistical computing, programming, and the UNIX environment
- Scripting with Python and Perl
- Statistical analysis and visualization with Python, MATLAB, and R
- Unix computing with Bash and Z shell
- High-performance computing and job scheduling with Torque/Maui, SGE, and LSF

Bioinformatics software
- Sequence/genome alignment: command-line BLAST, MUMmer, ClustalW, Muscle, Artemis/ACT
- Cluster analysis: OrthoMCL and R-based clustering packages
- Phylogenetics packages: PhyML, PAUP*, MrBayes, etc.

Creativity software
- Adobe Illustrator
- LaTeX
- HTML

Teaching Experience

- Lecturer, Introduction to Python, Scripps Institution of Oceanography, 2015–16
- Co-Supervisor of Ph.D. Student, KAUST, 2011–13
- Mentor of Undergraduate Students, Chisholm Lab, MIT, 2005–10
- Head Teaching Assistant, General Biochemistry, MIT, 2007
- Teaching Assistant, Introductory Biology, MIT, 2005
- Biology Tutor for Undergraduate Students, Boston Area, 2005–08
- Science Explorers Program, Fletcher-Maynard Academy and Cambridge Community Center, 2005–08
- Radio Talk Show Co-Host, *Biologue*, WMBR-FM Cambridge, 2005–08